

following paragraph:

5-2
Sequence homology (or identity) may moreover be determined using any suitable homology algorithm, using for example default parameters. Advantageously, the BLAST algorithm is employed, with parameters set to default values. The BLAST algorithm is known to those of skill in the art and is described, for example, in Altschul et al., 1990 (*J. Mol. Biol.* 215: 403).

On page 12, please delete the paragraph extending from lines 2-9 and insert the following paragraph:

5-3
BLAST (Basic Local Alignment Search Tool) is the heuristic search algorithm employed by the programs blastp, blastn, blastx, tblastn, and tblastx; these programs ascribe significance to their findings using the statistical methods of Karlin and Altschul (see Altschul et al., 1990 *J. Mol. Biol.* 215: 403) with a few enhancements. The BLAST programs were tailored for sequence similarity searching, for example to identify homologues to a query sequence. The programs are not generally useful for motif-style searching. For a discussion of basic issues in similarity searching of sequence databases, see Altschul et al. (1994).

On page 14, please delete the paragraph extending from lines 4-5 and insert the following paragraph:

5-4
More preferably, sequence comparisons are conducted using the simple BLAST search algorithm (Altschul et al., 1990 *J. Mol. Biol.* 215: 403).

In the Claims

Please **cancel** claims 1-7, 17-27, and 29.

Please **amend** claims 8-16 and 28 as follows: